

Table I (cont'd)

SEQ ID NO:	Name	Genbank Homology	Organism
103	2224-13	similar to ABC transporters	<i>C. elegans</i>
104	2098-3	Camguk	<i>D. melanogaster</i>
105	2101-9	UNC-89	<i>C. elegans</i>
106	2132-31	arginine kinase	<i>Homarus gammarus</i>
107	2141-51	casein kinase-II beta	<i>Oryctolagus cuniculus</i>
108	2178-18	diacylglycerol kinase eta	<i>Cricetinae</i>
109	2180-32	retinoid- and fatty acid-binding glycoprotein	<i>D. melanogaster</i>
110	2137-23	vitellogenin	<i>Aedes aegypti</i>
111	2144-14	nuclear localization signal spot 1	<i>Mus musculus</i>
112	2212-13	putative n- terminal acetyltransferase	<i>S. cerevisiae</i>
113	2212-27	clathrin associated protein AP47	<i>Drosophila grimshawi</i>
114	2223-28	O1 chloroquine-resistance protein	<i>Plasmodium falciparans</i>
115	2224-14	vitellogenin	<i>Athalia rosae</i>
116	2224-15	antigen NY-CO-3	<i>Homo sapiens</i>
117	2225-24	carbonic anhydrase	<i>C. elegans</i>
118	2225-58	yk500f6.3	<i>C. elegans</i>
119	2225-76	unknown	<i>Homo sapiens</i>
120	2224-86	BmP109 (cerebroside sulfate activator protein family)	<i>Bombyx mori</i>
121	2225-23	intersectin	<i>Homo sapiens</i>
122	2170-16	chemical-sense-related lipophilic-ligand-binding protein	<i>Phormia regina</i>
123	2176-2	olfactory receptor protein 2.4	<i>Danio rerio</i>
124	2212-63	olfactory receptor	<i>Xenopus laevis</i>
125	2224-77	inner mitochondrial membrane translocase Tim23	<i>Homo sapiens</i>
126	2225-12	sodium-dependent multi-vitamin transporter	<i>Rattus norvegicus</i>
127	2225-42	ribophorin I	<i>Rattus norvegicus</i>
128	2101-59	phosphate carrier protein	<i>C. elegans</i>
129	2132-38	proteinase inhibitor	<i>Locusta migratoria</i>
130	2174-72	HE4 protein	<i>Homo sapiens</i>
131	2211-48	spermatogenic cell/sperm-associated Tat-binding homologue	<i>Rattus norvegicus</i>
132	2110-23	Gcap1 gene product	<i>Mus musculus</i>
133	2116-64	toll protein	<i>D. melanogaster</i>
134	2124-3	tuberin (TSC2) gene	<i>Homo sapiens</i>
135	2178-55	RAS-like protein	<i>Gallus gallus</i>
136	2223-35	Rho1 gene product	<i>D. melanogaster</i>
137	2224-82	paxillin	<i>Homo sapiens</i>
138	2225-44	adenylyl cyclase-associated protein (CAP)	<i>Homo sapiens</i>
139	2225-80	adenylate kinase	<i>Gallus gallus</i>
140	2110-52	hydroxyproline-rich glycoprotein	<i>Phaseolus vulgaris</i>
141	2115-49	mitogen inducible gene mig-2	<i>Homo sapiens</i>
142	2116-5	F52H3.5	<i>C. elegans</i>
143	2172-89	12D3 antigen	<i>Babesia bovis</i>
144	2178-20	frameshift	<i>P. falciparum</i>
145	2178-81	KIAA0066	<i>Homo sapiens</i>

Table I (cont'd)

SEQ ID NO:	Name	Genbank Homology	Organism
146	2182-16	Y57G11C.4	<i>C. elegans</i>
147	2182-53	C16C10.5	<i>C. elegans</i>
148	2211-8	Unknown	<i>Homo sapiens</i>
149	2211-31	hypoetical protein	<i>Arabidopsis thaliana</i>
150	2223-54	ORF YNL207w	<i>S. cerevisiae</i>
151	2224-94	14.3 kDa perchloric acid soluble protein	<i>Capra hircus</i>
152	2225-36	EST clone	<i>C. elegans</i>
1719	2228-2	BIGH3	<i>H. sapiens</i>
1720	2228-5	H protein	<i>H. sapiens</i>
1721	2228-8	ubiquinol-cytochrome c reductase	<i>Schizosaccharomyces pombe</i>
1722	2228-11	similar to mitochondrial ATPase inhibitors	<i>C. elegans</i>
1723	2228-16	Putative enzyme	<i>E. coli</i>
1724	2228-18	Ribosomal protein L7A	<i>Drosophila</i>
1725	2228-22	Troponin-I wings up A	<i>Drosophila</i>
1726	2228-25	tls gene product	<i>E. coli</i>
1727	2228-27	YCR521 gene product	<i>Saccharomyces cerevisiae</i>
1728	2228-28	putative transport system permease protein	<i>E. coli</i>
1729	2228-32	SapA protein	<i>E. coli</i>
1730	2228-34	Putative protein	<i>Arabidopsis thaliana</i>
1731	2228-37	Ada	<i>E. coli</i>
1732	2228-39	Titin	<i>H. sapiens</i>
1733	2228-42	adenylosuccinate synthetase	<i>Mus musculus</i>
1734	2228-43	transfer RNA-Ala synthetase	<i>B. mori</i>
1735	2228-44	C4 zinc finger DNA-binding protein	<i>Drosophila</i>
1736	2228-48	heme A: farnesyltransferase	<i>H. sapiens</i>
1737	2228-51	URF 4L (aa 1-96)	<i>Drosophila</i>
1738	2228-53	DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE	<i>E. coli</i>
1739	2228-58	troponin-T	<i>Drosophila</i>
1740	2228-59	protein disulfide isomerase	<i>Drosophila</i>
1741	2228-63	orf, hypothetical protein	<i>E. coli</i>
1742	2228-66	ilvl polypeptide	<i>E. coli</i>
1743	2228-68	orf, hypothetical protein	<i>E. coli</i>
1744	2228-72	Respiratory nitrate reductase 1 alpha chain	<i>E. coli</i>
1745	2228-77	homolog of virulence factor	<i>E. coli</i>
1746	2228-84	ORF o164	<i>E. coli</i>
1747	2228-91	nuclear protein E3-3 orf1	<i>Rattus norvegicus</i>
1748	2245-66	Troponin C	<i>Drosophila</i>
1749	2245-70	Predicted secreted protein	<i>Plasmodium falciparum</i>
1750	2245-72	Cytochrome C-1	<i>H. sapiens</i>
1751	2245-75	rpoB	<i>Plasmodium falciparum</i>
1752	2245-78	sarco(endo)plasmic reticulum-type calcium ATPase	<i>Heliothis virescens</i>
1753	2246-31	Ras-related GTP-binding protein	<i>H. sapiens</i>
1754	2246-57	Similar to inositol 1,4,5-triphosphate receptor	<i>C. elegans</i>
1755	2246-61	reverse transcriptase-like protein	<i>Aedes aegypti</i>
1756	2247-13	polyprotein	<i>Drosophila</i>

Table I (cont'd)

SEQ ID NO:	Name	Genbank Homology	Organism
1757	2247-14	ORF2 for putative reverse transcriptase	<i>Drosophila</i>
1758	2247-42	Asparaginyl tRNA Synthetase	<i>H. sapiens</i>
1759	2247-44	calcium binding protein	<i>Drosophila</i>
1760	2247-58	similar to Fibronectin type III domain	<i>C. elegans</i>
1761	2247-62	reverse transcriptase	<i>Drosophila</i>
1762	2247-65	gag-like protein	<i>Culex pipiens</i>
1763	2247-79	L-3-phosphoserine phosphatase	<i>H. sapiens</i>
1764	2247-80	esterase E4	<i>Myzus persicae</i>
1765	2247-89	Similar to aldehyde dehydrogenase	<i>C. elegans</i>
1766	2248-76	O-44 protein	<i>Rattus sp.</i>
1767	2248-85	cDNA isolated for this protein using a monoclonal antibody directed against the p27k prosomal protein	<i>H. sapiens</i>
1768	2249-3	Projectin	<i>Drosophila</i>
1769	2249-5	ORF_ID:o312#14	<i>E. coli</i>
1770	2249-9	Heat shock protein 60	<i>Culicoides variipennis</i>
1771	2249-11	enigma protein	<i>H. sapiens</i>
1772	2249-12	alpha,alpha-trehalose glucohydrolase	<i>Oryctolagus cuniculus</i>
1773	2249-13	small GTP binding protein	<i>Drosophila</i>
1774	2249-14	Spermidine/putrescine transport system permease	<i>E. coli</i>
1775	2249-19	nueroendocrine-specific protein C	<i>H. sapiens</i>
1776	2249-21	a-agglutinin core subunit	<i>Saccharomyces cerevisiae</i>
1777	2249-24	KIAA0337	<i>H. sapiens</i>
1778	2249-34	su(wa) protein	<i>Drosophila</i>
1779	2249-42	regulator of kdp operon	<i>E. coli</i>
1780	2249-59	No definition line found	<i>C. elegans</i>
1781	2249-60	proline oxidase	<i>Drosophila</i>
1782	2249-62	Formate acetyltransferase	<i>E. coli</i>
1783	2249-70	similar to HECT-domain	<i>C. elegans</i>
1784	2249-75	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE	<i>E. coli</i>
1785	2249-77	Hypothetical 38.5 kd protein in agal-mtr intergenic region precursor	<i>E. coli</i>
1786	2249-85	D4L	<i>Variola virus</i>
1787	2249-87	similar to isocitrate dehydrogenase	<i>C. elegans</i>
1788	2250-6	Fii (head-tail joining;117)	<i>Bacteriophage Lambda</i>
1789	2250-7	possible NAGC-like transcriptional regulator	<i>E. coli</i>
1790	2250-10	cysteine string protein	<i>Bos taurus</i>
1791	2250-13	Tol B protein	<i>E. coli</i>
1792	2250-14	6-phosphogluconate dehydratase	<i>E. coli</i>
1793	2250-15	6-phosphogluconate dehydratase	<i>E. coli</i>
1794	2250-22	PSST subunit of the NADH: ubiquinone oxidoreductase	<i>Bos taurus</i>
1795	2250-30	sol i 3 antigen	<i>Solenopsis invicta</i>
1796	2250-36	predicted using Genefinder; similar to tRNA synthetases class I (E and Q	<i>C. elegans</i>
1797	2250-37	PNP	<i>H. sapiens</i>
1798	2250-42	ORF_ID:o331#2	<i>E. coli</i>
1799	2250-44	Extensin	<i>E. coli</i>

Table I (cont'd)

SEQ ID NO.	Name	Genbank Homology	Organism
1800	2250-47	ORF o654	<i>E. coli</i>
1801	2250-48	Gcap1 gene product	<i>Mus musculus</i>
1802	2250-52	similar to human MLH1 on chromosome 3p21	<i>Mus musculus</i>
1803	2250-53	Hypothetical 27.6 kd protein in hpt-panD intergenic region.	<i>E. coli</i>
1804	2250-58	UmuC protein	<i>E. coli</i>
1805	2250-61	dJ134E15.1 (Blimp-1	<i>H. sapiens</i>
1806	2250-63	ribosomal protein L23-related product homolog	<i>Rattus rattus</i>
1807	2250-65	hypothetical protein MJ1143	<i>E. coli</i>
1808	2250-68	HI0025 homolog	<i>E. coli</i>
1809	2250-77	R34094_1	<i>H. sapiens</i>
1810	2250-78	erythrocyte binding protein	<i>Plasmodium yoelii</i>
1811	2250-79	fosmidomycin resistance protein	<i>E. coli</i>
1812	2250-81	cyclophilin 1	<i>Drosophila</i>
1813	2250-83	putative glutamine synthetase	<i>E. coli</i>
1814	2251-3	J (tail:host specificity;1132)	<i>Bacteriophage Lambda</i>
1815	2251-5	Molybdopterin biosynthesis MoeB protein	<i>E. coli</i>
1816	2251-6	Fo-ATP synthase subunit b	<i>Drosophila</i>
1817	2251-9	citrate lyase alpha chain	<i>E. coli</i>
1818	2251-10	cuticle protein ACP65A	<i>Drosophila</i>
1819	2251-13	H repeat-associated protein in rhsC 3'region (orf-h3	<i>E. coli</i>
1820	2251-20	glycine-rich protein	<i>Arabidopsis thaliana</i>
1821	2251-23	2-oxoglutarate dehydrogenase precursor	<i>H. sapiens</i>
1822	2251-29	NFX1	<i>H. sapiens</i>
1823	2251-32	ebgR product, repressor	<i>E. coli</i>
1824	2251-41	neural protein	<i>Drosophila</i>
1825	2251-45	similar to unidentified ORF	<i>E. coli</i>
1826	2251-46	NADH:ubiquinone oxidoreductase b17.2 subunit	<i>Bos taurus</i>
1827	2251-49	tyrosine kinase	<i>Drosophila</i>
1828	2251-50	coded for by <i>C. elegans</i> cDNA yk89e9.5	<i>C. elegans</i>
1829	2251-57	H (tail component;853)	<i>Bacteriophage Lambda</i>
1830	2251-60	Lysyl tRNA Synthetase	<i>Drosophila</i>
1831	2251-62	7,8-diamino-pelargonic acid aminotransferase	<i>E. coli</i>
1832	2251-64	actin related protein	<i>Drosophila</i>
1833	2252-6	discs-large tumor suppressor	<i>Drosophila</i>
1834	2252-16	S-adenosylmethionine decarboxylase	<i>E. coli</i>
1835	2252-17	F52H3.5	<i>E. coli</i>
1836	2252-21	translationally controlled tumor protein	<i>Oryctolagus cuniculus</i>
1837	2252-31	GTP binding protein	<i>Rattus rattus</i>
1838	2252-34	mitochondrial porin transcript 1	<i>Drosophila</i>
1839	2252-38	cuticle protein	<i>Manduca sexta</i>
1840	2252-39	Similarity to Rat CD63 antigen	<i>C. elegans</i>
1841	2252-41	similar to <i>S. cerevisiae</i> Lpg20p	<i>E. coli</i>
1842	2252-48	cut E	<i>E. coli</i>
1843	2252-61	Histone H3	<i>Spisula solidissima</i>
1844	2252-66	ea10 (ssb;122)	<i>Bacteriophage Lambda</i>
1845	2252-71	Mao C protein	<i>E. coli</i>

Table I (cont'd)

SEQ ID NO:	Name	Genbank Homology	Organism
1846	2252-72	miniparomyosin	<i>Drosophila</i>
1847	2252-73	pherophorin-S	<i>Volvox carteri</i>
1848	2252-80	cyclophilin	<i>Mus musculus</i>
1849	2252-84	alternate gene name yhhG	<i>E. coli</i>
1850	2222-20	nucleoporin Nup98	<i>rat</i>
1851	2222-21	hypothetical protein	<i>Escherichia coli</i>
1852	2222-36	ribosomal protein S11	<i>human</i>
1853	2222-39	hypothetical protein PFB0315w	<i>Plasmodium falciparans</i>
1854	2222-50	serine/threonine-specific protein k.	<i>Plasmodium falciparans</i>
1855	2222-58	hypothetical protein C25E10.9	<i>C. elegans</i>
1856	2222-64	transporting ATP synthase	<i>bovine</i>
1857	2222-94	tricarboxylate carrier	<i>rat</i>
1858	2218-95	anoxia upregulated protein	<i>Drosophila melanogaster</i>

Table II represents a variety of flea HMT nucleic acid molecules of the present invention. Also cited in Table II are nucleic acid molecules from other organisms which share the closest sequence identity with the cited HMT sequences of the present invention, as determined by a search through the BLAST network as described above.

TABLE II

SEQ ID NO	Name	GenBank Homology	Organism
171	2094-23	mitochondrian ATP synthase, alpha subunit	<i>Drosophila melanogaster</i>
172	2104-20	mitochondrial ATP synthase	<i>Drosophila melanogaster</i>
173	2105-14	ATP synthase gamma-subunit	<i>Homo sapiens</i>
174	2167-72	oligomycin sensitivity conferring protein	<i>Drosophila melanogaster</i>
175	2179-20	ATPase 6	<i>Drosophila melanogaster</i>
176	2193-60	ATP synthase subunit B	<i>Schizaphis graminum</i>
177	2229-41	ATP synthase alpha subunit	<i>D. melanogaster</i>
178	2231-35	9 kD basic protein	<i>D. melanogaster</i>
179	2231-47	ATP synthase alpha-subunit	<i>Bos taurus</i>
180	2232-95	mitochondrial ATP synthase subunit 9	<i>Homo sapiens</i>
181	2084-56	Late embryogenesis abundant protein	<i>Picea glauca</i>
182	2084-36	TGF-beta masking protein/stranded at second	<i>Drosophila melanogaster</i>
183	2086-2	Argonaute protein	<i>Arabidopsis thaliana</i>
184	2196-92	like Drosophila HMPB homeotic proboscipedia protein	<i>C. elegans</i>
185	2092-27	DMDHEM2	<i>Drosophila melanogaster</i>
186	2094-21	SeiD protein	<i>Drosophila melanogaster</i>
187	2106-11	Unr	<i>Rattus norvegicus</i>
188	2231-15	cno (canoe)	<i>D. melanogaster</i>
189	2230-79	ALR homologue	<i>D. melanogaster</i>
190	2232-42	saxophone serine-threonine kinase receptor	<i>D. melanogaster</i>
191	2232-68	selenophosphate synthetase	<i>D. melanogaster</i>
192	2088-11	MMTAX107, TAX responsive element binding protein	<i>Mus musculus</i>
193	2089-2	cs Dna J-1	<i>Cucumis sativus</i>
194	2090-7	Lethal (2) TID	<i>Drosophila melanogaster</i>
195	2102-33	monocytic leukaemia zinc finger protein	<i>homo sapiens</i>
196	2105-26	orf1 5' of EpoR	<i>Mus musculus</i>
197	2106-6	contains similarity to EGF-1	<i>C. elegans</i>
198	2106-9	HSP70 protein	<i>Ceratitis capitata</i>
199	2084-60	82 kD heat shock protein	<i>Drosophila pseudobscura</i>
200	2108-59	PAR domain protein	<i>Drosophila melanogaster</i>
201	2156-34	yk29g12.3	<i>C. elegans</i>
202	2161-17	segmentation protein	<i>Drosophila melanogaster</i>
203	2162-28	heat shock protein 70, hsp70A2	<i>Anopheles albimanus</i>
204	2187-18	Heat shock protein 70	<i>Anopheles albimanus</i>
205	2173-77	Heat shock protein hsp70	<i>D. melanogaster</i>

Table II (cont'd)

SEQ ID NO:	Name	GenBank Homology	Organism
206	2165-30	nucleolar protein	<i>Drosophila melanogaster</i>
207	2165-59	contains similarity to C4-type zinc fingers	<i>C. elegans</i>
208	2177-80	zinc finger protein	<i>Mus musculus</i>
209	2181-45	PAR domain protein 1	<i>Drosophila melanogaster</i>
210	2185-9	Heat shock protein-70	<i>Anopheles albimanus</i>
211	2185-82	segmentation protein	<i>Drosophila melanogaster</i>
212	2188-33	transcriptional repressor protein	<i>Drosophila melanogaster</i>
213	2203-18	Mastermind	<i>Drosophila virilis</i>
214	2205-82	high mobility group protein 1a	<i>Chironomus tentans</i>
215	2230-26	DNA repair protein	<i>D. melanogaster</i>
216	2230-71	homologue of seven in absentia	<i>Homo sapiens</i>
217	2230-89	nuclear speckle-type protein, SPOP	<i>Homo sapiens</i>
218	2230-96	heat shock protein	<i>D. melanogaster</i>
219	2231-7	hypothetical protein	<i>S.pombe</i>
220	2231-38	Rad51 homolog	<i>Bombyx mori</i>
221	2231-81	DNA repair protein	<i>D. melanogaster</i>
222	2232-2	cellular nucleic acid binding protein	<i>Xenopus laevis</i>
223	2234-63	heat shock protein 70	<i>Trichoplusia ni</i>
224	2232-77	actin-binding double-zinc-finger protein (abLIM)	<i>Homo sapiens</i>
225	2234-78	DNA-binding protein isoform I	<i>D. melanogaster</i>
226	2084-48	Allantoinase	<i>Rana catesbeiana</i>
227	2085-22	beta-glucuronidase	<i>E. coli</i>
228	2094-24	prolidase = peptidaseD/imidopeptidase	<i>Mus musculus</i>
229	2088-43	branched chain alpha-keto acid dehydrogenase E1-beta subunit	<i>Bos taurus</i>
230	2086-29	3-hydroxyisobutyrate dehydrogenase	<i>Dictyostelium discoideum</i>
231	2088-5	Rab 5c protein	<i>Canis familiaris</i>
232	2095-17	cytochrome P-450	<i>Heliothis virescens</i>
233	2102-16	carbamoyl phosphate synthetase II	<i>Plasmodium falciparans</i>
234	2102-48	NADPH cytochrome P450 reductase	<i>Musca domestica</i>
235	2104-15	branched chain alpha-keto acid dehydrogenase	<i>Rattus norvegicus</i>
236	2106-5	Metallothionein	<i>Strongylocentrotus purpuratus</i>
237	2106-47	peroxidoxin-1	<i>Dirofilaria immitis</i>
238	2107-17	tetracycline transporter-like protein	<i>Mus musculus</i>
239	2107-58	allergen Bla g 5 (glutathione-S-transferase)	<i>Blattella germanica</i>
240	2156-58	HAL-3 homologue	<i>Arabidopsis thaliana</i>
241	2195-90	aminoacylase-1	<i>Homo sapiens</i>
242	2171-55	NADPH—ferrihemoprotein reductase	<i>Drosophila melanogaster</i>
243	2169-30	hypothetical protein	<i>Synechocystis sp</i>
244	2169-52	insulin degrading enzyme	<i>Drosophila melanogaster</i>
245	2177-64	3-hydroxyisobutyrate dehydrogenase	<i>Rattus norvegicus</i>
246	2181-69	Endonexin	<i>Bos taurus</i>
247	2138-25	glutamate dehydrogenase	<i>Drosophila melanogaster</i>
248	2230-28	glutathione -S-transferase	<i>Anopheles gambiae</i>
249	2191-8	lactase-phlorizin hydrolase	<i>Rattus rattus</i>
250	2193-52	cytochrome P450	<i>Heliothis virescens</i>

Table II (cont'd)

SEQ ID NO	Name	GenBank Homology	Organism
251	2202-35	glutathione-S-transferase	<i>Anopheles gambiae</i>
252	2229-77	glutathione-S-transferase	<i>Anopheles gambiae</i>
253	2229-81	urate oxidase	<i>D. melanogaster</i>
254	2231-42	superoxide dismutase	<i>Cervus elaphus</i>
255	2232-74	allergen Bla g 5	<i>Blattella germanica</i>
256	2234-42	glutathione reductase family	<i>Musca domestica</i>
257	2087-8	cystic fibrosis transmembrane conductance regulator	<i>Homo sapiens</i>
258	2087-23	Nervous system antigen 2	<i>Drosophila melanogaster</i>
259	2091-56	adenosine triphosphatase	<i>Homo sapiens</i>
260	2094-20	sodium pump, alpha subunit	<i>Ctenocephalides felis</i>
261	2095-51	similar to Hrs	<i>C. elegans</i>
262	2103-24	N-methyl-D-aspartate receptor-associated protein	<i>Drosophila melanogaster</i>
263	2105-55	inward rectifying K channel	<i>Sus scrofa</i>
264	2105-63	EF-hand Ca ²⁺ binding protein p22	<i>Rattus norvegicus</i>
265	2106-62	Dents disease candidate gene product	<i>Homo sapiens</i>
266	2167-50	PKD1 (polycystic kidney disease 1)	<i>Fugu rubripes</i>
267	2185-37	copper-transporting ATPase	<i>Archaeoglobus fulgidus</i>
268	2193-29	TrkG Potassium transport protein	<i>E. coli</i>
269	2195-33	silicon transporter	<i>Cylindrotheca fusiformis</i>
270	2202-16	similarity to human sulfate anion transporter	<i>C. elegans</i>
271	2230-2	sulfate transporter	<i>Arabidopsis thaliana</i>
272	2230-69	mitochondrial porin	<i>D. melanogaster</i>
273	2231-22	muscarinic acetylcholine receptor	<i>D. melanogaster</i>
274	2231-24	p97 subunit of 15S Mg(2+)- ATPase	<i>Xenopus laevis</i>
275	2231-32	anion transporting ATPase	<i>Aquifex aeolicus</i>
276	2231-70	sulfate permease	<i>Schizosaccharomyces pombe</i>
277	2231-94	putative Na/H exchanger	<i>S.pombe</i>
278	2233-6	plasma membrane Ca ²⁺ -ATPase 2	<i>Mus musculus</i>
279	2233-24	chloride channel gene, CLIC2	<i>Homo sapiens</i>
280	2085-61	beta-type protein kinase C	<i>Bos taurus</i>
281	2089-20	cGMP-dependent protein kinase	<i>Drosophila melanogaster</i>
282	2092-12	Btk	<i>Homo sapiens</i>
283	2093-64	Receptor-like protein tyrosine phosphatase	<i>Drosophila melanogaster</i>
284	2095-31	frt (fms-related tyrosine kinase gene)	<i>Homo sapiens</i>
285	2094-58	casein kinase II beta	<i>Oryctolagus cuniculus</i>
286	2103-54	ORF YGL084c	<i>Saccharomyces cerevisiae</i>
287	2106-42	protein phosphatase epsilon subunit	<i>Homo sapiens</i>
288	2156-5	serine/threonine kinase	<i>Rattus norvegicus</i>
289	2157-95	cGMP-dependent protein kinase	<i>Drosophila melanogaster</i>
290	2165-80	ABL gene product	<i>Gallus gallus</i>
291	2165-63	diadenosine tetraphosphatase	<i>Homo sapiens</i>
292	2167-17	adenylate cyclase	<i>S. cerevisiae</i>
293	2177-44	serine/threonine kinase	<i>C. elegans</i>
294	2188-16	weakly similar to serine/threonine kinase	<i>C. elegans</i>
295	2191-60	carbohydrate kinase, pfkB family	<i>Archaeoglobus fulgidus</i>

Table II (cont'd)

SEQ ID NO:	Name	GenBank Homology	Organism
296	2195-22	protein kinase	<i>Drosophila melanogaster</i>
297	2196-30	calcium-dependent protein kinase	<i>A. thaliana</i>
298	2205-83	protein kinase/endoribonuclease (IRE1)	<i>Homo sapiens</i>
299	2205-87	receptor tyrosine phosphatase	<i>Hirudo medicinalis</i>
300	2229-11	magnesium-dependent calcium inhibitable phosphatase	<i>Bos taurus</i>
301	2229-29	phosphoglycerate kinase	<i>Schistosoma mansoni</i>
302	2229-74	pyruvate kinase	<i>D. melanogaster</i>
303	2230-55	serine/threonine specific protein phosphatase 4	<i>D. melanogaster</i>
304	2230-57	stress activated MAP kinase kinase 3	<i>D. melanogaster</i>
305	2231-64	alkaline phosphatase	<i>D. melanogaster</i>
306	2231-91	olynucleotide phosphorylase	<i>Yersinia enterocolitica</i>
307	2232-43	protein kinase PkwA	<i>Thermomonospora curvata</i>
308	2234-94	serine/threonine kinase ULK1	<i>Homo sapiens</i>
309	2085-18	Pyridoxamine phosphate oxidase	<i>C. elegans</i>
310	2094-13	sphingomyelin phosphodiesterase	<i>Mus musculus</i>
311	2105-47	apolipoprotein E receptor 2	<i>Homo sapiens</i>
312	2092-38	squalene synthetase	<i>Homo sapiens</i>
313	2094-25	fatty acid synthetase	<i>Rattus norvegicus</i>
314	2089-32	coproporphyrinogen oxidase	<i>Homo sapiens</i>
315	2085-46	HADHB mitochondrial trifunctional protein beta subunit	<i>Homo sapiens</i>
316	2104-56	pyridoxal kinase	<i>Homo sapiens</i>
317	2107-30	Phosphomevalonate kinase	<i>Homo sapiens</i>
318	2154-70	very-long chain acyl-CoA dehydrogenase	<i>Mus musculus</i>
319	2191-85	stearyl-CoA desaturase	<i>Cyprinus carpio</i>
320	2192-44	very-long-chain Acyl-CoA dehydrogenase	<i>Rattus norvegicus</i>
321	2195-55	Similar to LDL receptor-related protein	<i>C. elegans</i>
322	2229-82	lipase-3	<i>D. melanogaster</i>
323	2231-59	Phosphatidylethanolamine-binding protein	<i>Macaca fascicularis</i>
324	2233-25	similarity to yeast ethanolaminephosphotransferase	<i>C. elegans</i>
325	2233-41	cellular retinoic acid binding protein (mCRABP)	<i>Manduca sexta</i>
326	2087-61	allergen	<i>Lepidoglyphus destructor</i>
327	2087-41	chloroquine resistance candidate protein	<i>Plasmodium falciparum</i>
328	2089-51	Xenopus Bf B	<i>Xenopus laevis</i>
329	2086-58	repeat organellar protein	<i>Plasmodium falciparum</i>
330	2090-45	heat shock cognate protein	<i>Drosophila melanogaster</i>
331	2104-23	40 kDa heat shock chaperone protein	<i>Deinococcus</i>
332	2107-26	Luciferase	<i>Photuris pennsylvanica</i>
333	2162-46	F20D1.9	<i>C. elegans</i>
334	2162-49	PKR inhibitor P58	<i>Bos taurus</i>
335	2162-93	GroES homologue	<i>Rickettsia</i>
336	2171-46	NH2 terminus uncertain	<i>Leishmania tarentolae</i>
337	2089-10	beta adaptin	<i>Drosophila melanogaster</i>
338	2229-24	non-functional folate binding protein	<i>Homo sapiens</i>
339	2229-25	calmodulin B	<i>Halocynthia roretzi</i>

Table II (cont'd)

SEQ ID NO:	Name	GenBank Homology	Organism
340	2229-31	putative T1/ST2receptor binding protein	<i>C. elegans</i>
341	2229-36	alpha-crystallin cognate protein 25	<i>Plodia interpunctella</i>
342	2229-40	Defensin	<i>Apis mellifera</i>
343	2229-86	glutamate—ammonia ligase	<i>D. melanogaster</i>
344	2231-49	melanoma-associated antigen ME491	<i>Homo sapiens</i>
345	2231-76	histone C	<i>Drosophila virilis</i>
346	2232-65	translationally controlled tumor protein	<i>Oryctolagus cuniculus</i>
347	2232-84	Apyrase	<i>Aedes aegypti</i>
348	2232-85	KIAA0124	<i>Homo sapiens</i>
349	2233-59	Glutamine-dependent carbamoyl-phosphate synthase	<i>C. elegans</i>
350	2233-86	ANG12 precursor	<i>Anopheles gambiae</i>
351	2234-11	tissue specific secretory protein	<i>Pan troglodytes</i>
352	2234-76	methionine adenosyltransferase	<i>D. melanogaster</i>
353	2089-13	Synaptic vessicle protein 2 form B	<i>Rattus norvegicus</i>
354	2159-52	glycoprotein 56	<i>Rattus norvegicus</i>
355	2084-6	CLN3; homologue of the gene underlying Batten disease	<i>Mus musculus</i>
356	2085-10	Amphiphysin	<i>Gallus gallus</i>
357	2156-39	glycoprotein 55	<i>Rattus norvegicus</i>
358	2104-59	Transmembrane transporter	<i>Discopyge ommata</i>
359	2105-9	insect intestinal mucin II	<i>Trichoplusia ni</i>
360	2106-14	kinesin-like protein	<i>D. melanogaster</i>
361	2107-45	Lazarillo precursor	<i>Schistocerca americana</i>
362	2156-3	clathrin-associated protein	<i>Mus musculus</i>
363	2161-46	neural variant mena+ protein	<i>Mus musculus</i>
364	2171-92	Malvolio	<i>Drosophila melanogaster</i>
365	2175-18	homolog of SYT – synaptotagmin	<i>Mus musculus</i>
366	2177-10	GABA receptor subunit (Rdl)	<i>Aedes aegypti</i>
367	2181-10	neurexin IV	<i>Drosophila melanogaster</i>
368	2191-92	synaptic vessicle protein 2B	<i>Rattus norvegicus</i>
369	2229-18	Synaptic vessicle protein 2A	<i>Rattus norvegicus</i>
370	2194-38	gamma-subunit of mouse nerve growth factor	<i>Mus musculus</i>
371	2230-60	lin-7-C	<i>Rattus norvegicus</i>
372	2230-81	PDZ domain protein	<i>Homo sapiens</i>
373	2234-5	Gcap1 gene product	<i>Mus musculus</i>
374	2234-55	Gcap1 gene product	<i>Mus musculus</i>
375	2234-71	Gcap1 gene product	<i>Mus musculus</i>
376	2085-34	Liver-specific transport protein	<i>Rattus norvegicus</i>
377	2087-15	polyspecific organic cation transporter	<i>Homo sapiens</i>
378	2204-80	transmembrane transporter	<i>Discopyge ommatta</i>
379	2093-39	liver-specific transport protein	<i>Rattus norvegicus</i>
380	2093-46	similar to monocarboxylate transporter family	<i>C. elegans</i>
381	2092-22	similar to matrin F/G	<i>C. elegans</i>
382	2103-50	Unknown	<i>Drosophila melanogaster</i>
383	2103-51	organic cation transporter	<i>Rattus norvegicus</i>
384	2197-35	renal organic cation transporter	<i>Oryctolagus cuniculus</i>
385	2156-17	sulfate anion transporter	<i>Manduca sexta</i>

Table II (cont'd)

SEQ ID NO:	Name	GenBank Homology	Organism
386	2166-84	LX1	<i>Mus musculus</i>
387	2167-94	MCT (monocarboxylate transporter)	<i>Homo sapiens</i>
388	2196-83	renal organic cation transporter	<i>Oryctolagus cuniculus</i>
389	2229-83	similarity to monocarboxylate transporter 1	<i>C. elegans</i>
390	2231-89	Golgi 4-transmembrane spanning transporter MTP	<i>Mus musculus</i>
391	2158-8	phosphate carrier protein	<i>C. elegans</i>
392	2085-14	ADP/ATP translocase	<i>Drosophila melanogaster</i>
393	2085-17	Na ⁺ -dependent inorganic phosphatase cotransporter	<i>Drosophila melanogaster</i>
394	2088-38	ADP/ATP translocase	<i>Bos taurus</i>
395	2092-50	ADP/ATP translocase	<i>Drosophila melanogaster</i>
396	2104-21	Na(+)-dependent inorganic phosphate cotransporter	<i>Drosophila melanogaster</i>
397	2121-55	phosphate carrier protein	<i>C. elegans</i>
398	2105-64	phosphate carrier protein	<i>Homo sapiens</i>
399	2102-6	ZK512.6	<i>C. elegans</i>
400	2108-27	mitochondrial phosphate carrier protein	<i>Homo sapiens</i>
401	2194-63	mitochondrial phosphate transporter	<i>Rattus norvegicus</i>
402	2196-14	phosphate/triose-phosphate translocator precursor	<i>C. elegans</i>
403	2204-11	EST clone	<i>D. melanogaster</i>
404	2085-16	Chymotrypsin I	<i>Anopheles gambiae</i>
405	2085-54	Chymotrypsin II	<i>Anopheles gambiae</i>
406	2086-12	Plasminogen	<i>Homo sapiens</i>
407	2086-18	Trypsin eta	<i>Drosophila melanogaster</i>
408	2090-21	Trypsin	<i>Manduca sexta</i>
409	2092-15	Alp1	<i>Cochliobolus carbonum</i>
410	2102-11	vitellin-degrading protease	<i>Bombyx mori</i>
411	2102-17	Chymotrypsin II	<i>Anopheles gambiae</i>
412	2102-51	chymotrypsin -like protease	<i>Anopheles gambiae</i>
413	2103-31	Beta trypsin	<i>Drosophila erecta</i>
414	2107-22	Factor IX	<i>Rattus norvegicus</i>
415	2108-29	Trypsin	<i>Anopheles stephensi</i>
416	2157-15	Trypsin	<i>Choristoneura fumiferana</i>
417	2160-34	Aminopeptidase	<i>Synechocystis</i>
418	2160-36	E01G6.1	<i>C. elegans</i>
419	2103-62	plasminogen activator inhibitor 2	<i>Mus musculus</i>
420	2167-36	factor IX	<i>Oryctolagus cuniculus</i>
421	2167-67	Alp1	<i>Cochliobolus carbonum</i>
422	2169-51	Trypsin	<i>Aedes aegypti</i>
423	2181-27	Chymotrypsin BII	<i>Penaeus vannamei</i>
424	2185-69	plasma prekallikrein	<i>Homo sapeins</i>
425	2187-20	pre-procathepsin L	<i>Paragonimus westermani</i>
426	2188-45	vitellin-degrading protease	<i>Bombyx mori</i>
427	2192-91	late trypsin precourser	<i>Culex pipiens quinquefasciatus</i>
428	2196-10	SPC2	<i>Branchiostoma californiensis</i>
429	2196-88	Trypsin	<i>Anopheles stephensi</i>

Table II (cont'd)

SEQ ID NO:	Name	GenBank Homology	Organism
430	2204-9	carnitine/choline acetyltransferase	<i>C. elegans</i>
431	2229-7	iota trypsin	<i>D. melanogaster</i>
432	2229-22	Trypsin	<i>Anopheles gambiae</i>
433	2229-89	Trypsin	<i>Anopheles gambiae</i>
434	2229-94	late trypsin precursor	<i>Culex pipiens quinquefasciatus</i>
435	2230-59	Chymotrypsin 1	<i>Anopheles gambiae</i>
436	2230-67	carboxypeptidase A	<i>Drosophila heteroneura</i>
437	2231-62	aminopeptidase N	<i>Sus scrofa</i>
438	2231-74	limulus factor C serine protease	<i>Tachyplesus tridentatus</i>
439	2232-15	cysteine proteinase	<i>Sitophilus zeamais</i>
440	2232-25	Carboxypeptidase	<i>Simulium vitatum</i>
441	2232-33	putative aspartic protease	<i>Brassica oleracea</i>
442	2233-46	aminopeptidase N	<i>Pleuronectes americanus</i>
443	2233-85	chymotrypsin 1	<i>Anopheles gambiae</i>
444	2233-90	Trypsin	<i>Anopheles stephensi</i>
445	2233-94	preprochymotrypsin 1	<i>Penaeus vannamei</i>
446	2234-29	chymotrypsin-like protease precursor	<i>Aedes aegypti</i>
447	2234-58	Putative	<i>C. elegans</i>
448	2234-61	carboxylesterase precursor	<i>Aphis gossypii</i>
449	2234-68	serine protease inhibitor I	<i>Schistocerca gregaria</i>
450	2084-35	Integral membrane protein	<i>Mus musculus</i>
451	2086-45	similar to beta-ureidopropionase of Rat	<i>C. elegans</i>
452	2087-54	Cyclin	<i>Mus musculus</i>
453	2088-22	Esp 8	<i>Mus musculus</i>
454	2091-16	contains similarity to EGF-like domains	<i>C. elegans</i>
455	2091-29	multiple exostosis-like protein	<i>Homo sapiens</i>
456	2091-30	apoptosis 1 inhibitor	<i>Drosophila melanogaster</i>
457	2092-33	KIAA0023 (putative oncogene)	<i>Homo sapiens</i>
458	2095-35	G coupled receptor	<i>C. elegans</i>
459	2095-3	Go (heterotrimeric guanyl nucleotide binding protein alpha subunit)	<i>Manduca sexta</i>
460	2085-4	gp 150 protein	<i>Drosophila melanogaster</i>
461	2103-28	leukotriene A4 hydrolase	<i>Rattus sp.</i>
462	2105-62	putitive orf	<i>Homo sapiens</i>
463	2107-6	activator protein	<i>Drosophila melanogaster</i>
464	2107-28	platelet-endothelial tetraspan antigen 3	<i>Homo sapiens</i>
465	2189-3	oligopeptidase A (prIC)	<i>Haemophilis influenzae</i>
466	2156-54	fibroblast growth factor receptor	<i>Xenopus laevis</i>
467	2160-92	contains similarity to EGF-like domains	<i>C. elegans</i>
468	2160-65	weak similarity to the drosophila hyperplastic disc protein	<i>C. elegans</i>
469	2165-53	inositol triphosphate receptor	<i>Rattus norvegicus</i>
470	2166-22	placental protein 11	<i>Homo sapiens</i>
471	2166-92	elongation factor 1 alpha-like	<i>Drosophila melanogaster</i>
472	2181-34	DSch	<i>Drosophila melanogaster</i>
473	2192-65	STAM, signal transducing adaptor molecule	<i>Homo sapiens</i>
474	2194-24	ATPases associated with various cellular activities (AAA family)	<i>Arabidopsis thaliana</i>

Table II (cont'd)

SEQ ID.NO:	Name	GenBank Homology	Organism
475	2196-75	similar to cell division control protein	<i>C. elegans</i>
476	2230-38	EST clone	<i>S. cerevisiae</i>
477	2230-39	NTPase	<i>D. melanogaster</i>
478	2230-66	adenylyl cyclase aggregation protein	<i>Dictyostelium discoideum</i>
479	2230-80	sphingomyelin phosphodiesterase	<i>C. elegans</i>
480	2231-29	nuclear antigen H731	<i>Homo sapiens</i>
481	2231-40	suppressor of actin mutation 2	<i>Homo sapiens</i>
482	2231-66	DET1	<i>Arabidopsis thaliana</i>
483	2232-7	Calreticulin	<i>D. melanogaster</i>
484	2232-38	activator protein	<i>D. melanogaster</i>
485	2232-69	ornithine decarboxylase	<i>Gallus gallus</i>
486	2233-32	similar bHLH-PAS	<i>D. melanogaster</i>
487	2233-45	rab1	<i>D. melanogaster</i>
488	2234-2	C10A gene product	<i>Mus musculus</i>
489	2234-72	QM homolog	<i>D. melanogaster</i>
490	2084-17	Integral membrane protein	<i>Herpesvirus-2</i>
491	2091-4	endomembrane protien EMP70 precursor isolog	<i>Arabidopsis thaliana</i>
492	2102-45	Ylr251wp	<i>Saccharomyces cerevisiae</i>
493	2162-68	220 kDa silk protein	<i>Chironomus thummi</i>
494	2160-47	precursor HT7 protein	<i>Gallus gallus</i>
495	2161-12	peritrophin 95 precursor	<i>Lucilia cuprina</i>
496	2161-15	yk86g11.5	<i>C. elegans</i>
497	2171-12	51A surface protein	<i>Paramecium tetraurelia</i>
498	2173-18	hypothetical – mitochondrial membrane transport protein	<i>Schizosaccharomyces pombe</i>
499	2087-32	est sequence	<i>C. elegans</i>
500	2091-19	Similar to P. aeruginosa hypothetical protein	<i>C. elegans</i>
501	2192-86	tyrosine kinase	<i>Drosophila melanogaster</i>
502	2086-42	M04B2.4	<i>C. elegans</i>
503	2088-16	glycoprotein 330	<i>C. elegans/Human</i>
504	2088-39	EST sequence	<i>Arabidopsis thaliana</i>
505	2088-57	Yer 126cp	<i>Saccharomyces cerevisiae</i>
506	2089-25	similar to S. cerevisiae hypothetical protein YKL166	<i>C. elegans</i>
507	2090-3	EST sequence	<i>Saccharomyces cerevisiae</i>
508	2090-53	EST sequence	<i>C. elegans</i>
509	2095-20	Chloroplast ORF	<i>Marchantia polymorpha</i>
510	2102-28	similar to S. cerevisiae hypothetical protein YKL166	<i>C. elegans</i>
511	2102-55	D1054.3	<i>C. elegans</i>
512	2102-58	ZC513.5 gene product	<i>C. elegans</i>
513	2105-44	E 1087 protein	<i>Saccharomyces cerevisiae</i>
514	2109-24	F11C1.5	<i>C. elegans</i>
515	2154-21	disulfide-like protein	<i>Acanthamoeba castellanii</i>
516	2156-6	ZK470.1	<i>C. elegans</i>
517	2156-18	BIIIA3	<i>Ovis aries</i>
518	2156-27	AFR1	<i>S. cerevisiae</i>
519	2165-94	COS41.8	<i>Ciona intestinalis</i>

Table II (cont'd)

SEQ ID NO:	Name	GenBank Homology	Organism
520	2167-65	EST sequence, function unknown	<i>C. elegans</i>
521	2171-93	KIAA0160	<i>Homo sapiens</i>
522	2175-45	ORF YJR83.18	<i>S. cerevisiae</i>
523	2185-66	rps4	<i>Plasmodium falciparum</i>
524	2195-40	C27C12.4	<i>C. elegans</i>
525	2196-20	glycoprotein A	<i>Pneumocystis carinii</i>
526	2205-89	BKRF1 encodes EBNA-1 protein	Epstein Barr virus
527	2229-19	D4L	Variola virus
528	2230-35	KIAA0747	<i>Homo sapiens</i>
529	2231-8	I3	<i>Mus musculus</i>
530	2231-78	unknown protein	<i>Arabidopsis thaliana</i>
531	2232-49	Similarity to Yeast hypothetical 52.9 KD protein	<i>C. elegans</i>
532	2232-52	tetratricopeptide repeat protein (tpr2)	<i>Homo sapiens</i>
533	2233-5	similar to <i>Saccharomyces cerevisiae</i> SCD6 protein	<i>C. elegans</i>
534	2233-22	cDNA EST yk486b9.3	<i>C. elegans</i>
535	2233-93	CDC27Dm	<i>D. melanogaster</i>
536	2084-34	immune suppressor/V-ATPase 115 kDa subunit	<i>Mus musculus</i>
537	2086-30	V-ATPase A-subunit	<i>Aedes aegypti</i>
538	2087-45	H+ ATPase	<i>Drosophila melanogaster</i>
539	2088-55	40-kDa-V-ATPase subunit	<i>Manduca sexta</i>
540	2088-62	vacuolar ATPase subunit A	<i>Drosophila melanogaster</i>
541	2091-26	proton-ATPase-like protein	<i>Homo sapiens</i>
542	2091-31	vacuolar ATPase subunit A	<i>Drosophila melanogaster</i>
543	2092-20	vacuolar ATPase 115 kDa subunit	<i>Homo sapiens</i>
544	2095-18	similar to <i>S. cerevisiae</i> vacuolar H(+)-ATPase 54 kD subunit	<i>C. elegans</i>
545	2095-54	H (+)-transporting ATPase subunit B	<i>Manduca sexta</i>
546	2108-8	similar to <i>S. cerevisiae</i> 54 kDa V-ATPase subunit	<i>C. elegans</i>
547	2154-36	V-ATPase subunit E	<i>Drosophila melanogaster</i>
548	2154-76	V-ATPase subunit A (new fragment)	<i>Aedes aegypti</i>
549	2166-32	V-ATPase C subunit	<i>Drosophila melanogaster</i>
550	2166-33	vacuolar (V-type) H(+)-ATPase B subunit	<i>Helicoverpa virescens</i>
551	2166-90	beta subunit of ATPase	<i>Schizaphis graminum</i>
552	2161-5	ATPase I	<i>Plasmodium falciparum</i>
553	2171-24	similar to V-ATPase 116kd subunit	<i>C. elegans</i>
554	2169-82	V-ATPase subunit E	<i>Drosophila melanogaster</i>
555	2187-36	V-ATPase membrane sector associated protein M8-9	<i>Homo sapiens</i>
556	2188-91	V-ATPase subunit A	<i>Candida tropicalis</i>
557	2230-88	vacuolar ATPase G subunit	<i>Manduca sexta</i>
558	2232-61	V-ATPase subunit C	<i>D. melanogaster</i>
559	2086-52	Penelope transposable element ORF	<i>Drosophila virilis</i>
560	2103-2	genome polyprotein gene product	Plum pox virus
561	2106-8	pol protein	Human T-cell lymphotropic virus type 2
562	2108-41	reverse transcriptase, Doc retroposon	<i>Drosophila melanogaster</i>

Table II (cont'd)

SEQ ID NO:	Name	GenBank Homology	Organism
563	2202-28	Polyprotein	<i>Hepatitis virus C</i>
564	2165-95	DNA polymerase	<i>Choristoneura biennis entomopoxvirus</i>
565	2169-81	reverse transcriptase	<i>Drosophila melanogaster</i>
566	2181-36	reverse transcriptase	<i>Anopheles gambiae</i>
1416	2240-4	alpha-L-fucosidase precursor	<i>Homo sapiens</i>
1417	2240-11	estrogen related receptor alpha	<i>Mus musculus</i>
1418	2240-14	NADH:ubiquinone oxidoreductase 51-kD subunit	<i>Homo sapiens</i>
1419	2240-17	peritrophin 1	<i>Anopheles gambiae</i>
1420	2240-19	small GTPase rac1b	<i>Homo sapiens</i>
1421	2240-23	Symplekin	<i>Homo sapiens</i>
1422	2240-26	ribosomal protein L30	<i>Bos taurus</i>
1423	2240-28	60S Ribosomal Protein RPL10A	<i>Homo sapiens</i>
1424	2240-29	KIN17 protein	<i>D. melanogaster</i>
1425	2240-31	eukaryotic initiation factor 4 gamma	<i>Homo sapiens</i>
1426	2240-38	ornithine decarboxylase antizyme	<i>D. melanogaster</i>
1427	2240-44	electron transfer flavoprotein	<i>Rattus norvegicus</i>
1428	2240-53	EST clone	<i>C. elegans</i>
1429	2240-55	glutathione reductase family	<i>Musca domestica</i>
1430	2240-58	chymotrypsin-like serine protease	<i>C. felis</i>
1431	2240-63	ferritin subunit 1	<i>D. melanogaster</i>
1432	2240-64	vacuolar ATPase subunit B	<i>D. melanogaster</i>
1433	2240-66	chaperonin containing TCP-1 delta	<i>Fugu rubripes</i>
1434	2240-70	1-acyl-glycerol-3-phosphate acyltransferase	<i>Zea mays</i>
1435	2240-71	EST clone AL021106	<i>D. melanogaster</i>
1436	2240-72	376aa long hypothetical dehydrogenase	<i>Pyrococcus horikoshii</i>
1437	2240-77	chymotrypsin-like serine protease	<i>C. felis</i>
1438	2240-80	EST clone	<i>C. elegans</i>
1439	2240-83	chymotrypsin-like serine protease	<i>C. felis</i>
1440	2240-90	cytochrome P450	<i>D. melanogaster</i>
1441	2240-93	enhancer-trap-locus-1	<i>Mus musculus</i>
1442	2240-94	glycerol-3-phosphate dehydrogenase	<i>Ceratitis capitata</i>
1443	2241-3	FS-H precursor	<i>Ctenocephalides felis</i>
1444	2241-5	trypsin-like serine protease	<i>Ctenocephalides felis</i>
1445	2241-7	myospheroid protein	<i>D. melanogaster</i>
1446	2241-10	Sam50	<i>D. melanogaster</i>
1447	2241-12	NADH dehydrogenase subunit 2	<i>Chorthippus parallelus</i>
1448	2241-15	putative protein	<i>Arabidopsis thaliana</i>
1449	2241-16	contains EGF-like repeats	<i>C. elegans</i>
1450	2241-20	Gcap1 gene product	<i>Mus musculus</i>
1451	2241-25	Na(+)-dependent inorganic phosphate cotransporter	<i>D. melanogaster</i>
1452	2241-31	D4L	<i>Variola virus</i>
1453	2241-36	plenty-of-prolines-101; POP101; SH3-philo-protein	<i>Mus musculus</i>
1454	2241-40	EF-1-alpha	<i>D. melanogaster</i>

Table II (cont'd)

SEQ ID NO.	Name	GenBank Homology	Organism
1455	2241-44	F1-ATP synthase epsilon-subunit	<i>Ipomoea batatas</i>
1456	2241-54	ribosomal protein S28	<i>Homo sapiens</i>
1457	2241-55	Y-box protein	<i>D. melanogaster</i>
1458	2241-56	short-chain alcohol dehydrogenase	<i>Homo sapiens</i>
1459	2241-59	contains 3 cysteine rich repeats	<i>C. elegans</i>
1460	2241-60	muscle type phosphofructokinase	<i>Canis familiaris</i>
1461	2241-61	Heat shock protein 82	<i>Mus musculus</i>
1462	2241-65	chymotrypsin-like protease	<i>C. felis</i>
1463	2241-66	Oligosaccharyltransferase subunit	<i>D. melanogaster</i>
1464	2241-70	EST clone	<i>D. melanogaster</i>
1465	2241-72	failed axon connections protein	<i>D. melanogaster</i>
1466	2241-74	Enolase	<i>Hymenolepis diminuta</i>
1467	2241-78	multiple exostosis 2 protein	<i>Mus musculus</i>
1468	2241-80	Protein on Ecdysone Puffs	<i>D. melanogaster</i>
1469	2241-82	paramyosin	<i>D. melanogaster</i>
1470	2241-83	beta-tubulin	<i>Bombyx mori</i>
1471	2241-84	natural killer cell enhancing factor	<i>Cyprinus carpio</i>
1472	2241-86	similar to MYOTUBULARIN-RELATED PROTEIN	<i>Homo sapiens</i>
1473	2241-87	Renin	<i>Rattus norvegicus</i>
1474	2241-90	Myophilin	<i>Echinococcus multilocularis</i>
1475	2243-10	alpha-actinin	<i>D. melanogaster</i>
1476	2243-11	monocarboxylate transporter	<i>Homo sapiens</i>
1477	2243-13	yk278a10.3	<i>C. elegans</i>
1478	2243-15	selenium donor protein	<i>Homo sapiens</i>
1479	2243-18	acetyl-CoA synthetase	<i>D. melanogaster</i>
1480	2243-20	cytochrome P450 CYP12A3	<i>Musca domestica</i>
1481	2243-22	NADH dehydrogenase subunit 4	<i>Anopheles arabiensis</i>
1482	2243-27	Polyubiquitin	<i>Cricetulus griseus</i>
1483	2243-28	Moesin	<i>D. melanogaster</i>
1484	2243-31	QM protein	<i>Bombyx mandarina</i>
1485	2243-32	Sec23 protein	<i>Homo sapiens</i>
1486	2243-37	truncated protein	<i>S. cerevisiae</i>
1487	2243-38	Projectin	<i>D. melanogaster</i>
1488	2243-39	Unknown	<i>Homo sapiens</i>
1489	2243-41	similar to enoyl-CoA hydratase	<i>C. elegans</i>
1490	2243-45	similar to dehydrogenase	<i>C. elegans</i>
1491	2243-46	trypsin-like serine protease	<i>C. felis</i>
1492	2243-48	Merlin	<i>Rattus norvegicus</i>
1493	2243-52	GTP-specific succinyl-CoA synthetase beta subunit	<i>Homo sapiens</i>
1494	2243-53	sod protein (superoxide dismutase)	<i>Drosophila virilis</i>
1495	2243-54	trypsin-like serine protease	<i>C. felis</i>
1496	2243-61	chymotrypsin-like serine protease	<i>C. felis</i>
1497	2243-66	Tag B	<i>Dictyostelium discoideum</i>
1498	2243-67	hypothetical protien	<i>Arabidopsis thaliana</i>
1499	2243-68	heat shock cognate protein 70	<i>Trichoplusia ni</i>

Table II (cont'd)

SEQ ID NO:	Name	GenBank Homology	Organism
1500	2243-72	TRIP-1 homologue	<i>D. melanogaster</i>
1501	2243-73	cytosolic NADP-dependent isocitrate dehydrogenase	<i>Microtis mexicanis</i>
1502	2243-86	progesterone-induced protein	<i>Oryctolagus cuniculus</i>
1503	2243-87	Bmsqd-2	<i>Bombyx mori</i>
1504	2243-91	sodium/iodide symporter	<i>Homo sapiens</i>
1505	2243-92	ORF2	<i>Acidianus ambivalens</i>
1506	2243-94	lysosomal beta-galactosidase	<i>Felis cattus</i>
1507	2244-12	tropomyosin isoform 127	<i>D. melanogaster</i>
1508	2244-19	KIAA0181	<i>Homo sapiens</i>
1509	2244-23	plasma membrane calcium ATPase isoform 1	<i>Homo sapiens</i>
1510	2244-29	NADH dehydrogenase	<i>Bos taurus</i>
1511	2244-44	glutamate dehydrogenase	<i>D. melanogaster</i>
1512	2244-54	spliceosomal protein	<i>D. melanogaster</i>
1513	2244-59	ciliary body glutathione peroxidase	<i>Bos taurus</i>
1514	2244-61	pyridoxal-phosphate-dependent aminotransferases	<i>C. elegans</i>
1515	2244-64	Unknown	<i>Rattus norvegicus</i>
1516	2244-69	trypsin-like serine protease	<i>C. felis</i>
1517	2244-71	peritrophin 1	<i>Anopheles gambiae</i>
1518	2244-75	NADH dehydrogenase subunit 5	<i>Anopheles gambiae</i>
1519	2244-84	microsomal epoxide hydrolase	<i>Rattus norvegicus</i>
1520	2244-86	C54G7.2 gene product	<i>C. elegans</i>
1521	2244-91	Aminopeptidase N	<i>Plutella xylostella</i>
1522	2253-2	cytochrome C oxidase	<i>H. sapiens</i>
1523	2253-13	Initiation factor 5A	<i>Gallus gallus</i>
1524	2253-14	protein phosphatase type 2A catalytic subunit	<i>Bos taurus</i>
1525	2253-16	myosin light chain 2	<i>D. melanogaster</i>
1526	2253-18	cDNA EST yk462d1.5	<i>C. elegans</i>
1527	2253-19	ribosomal protein S10	<i>H. sapiens</i>
1528	2253-24	aspartyl(asparaginyl)beta-hydroxylase, HAAH	<i>H. sapiens</i>
1529	2253-27	larval and adult myosin heavy chain	<i>D. melanogaster</i>
1530	2253-33	nervous system antigen 2	<i>D. melanogaster</i>
1531	2253-36	dJ366N23.2	<i>H. sapiens</i>
1532	2253-40	hrp48.1	<i>D. melanogaster</i>
1533	2253-42	ZnT-1	<i>Mus musculus</i>
1534	2253-43	aminopeptidase N	<i>Manduca sexta</i>
1535	2253-56	Profilin	<i>D. melanogaster</i>
1536	2253-59	T26A5.	<i>H. sapiens</i>
1537	2253-68	NADH-ubiquinone oxidoreductase 42 kDa subunit	<i>D. melanogaster</i>
1538	2253-78	glycine-rich protein	
1539	2253-81	5'-nucleotidase	<i>H. sapiens</i>
1540	2253-86	glutathione S-transferase	<i>Anopheles gambiae</i>
1541	2253-87	ferritin subunit 1	<i>D. melanogaster</i>
1542	2253-92	myosin light chain 2	<i>D. melanogaster</i>
1543	2253-94	xylose-proton symport	<i>E. coli</i>
1544	2254-4	mature-parasite-infected erythrocyte surface antigen	<i>P. falciparum</i>

Table II (cont'd)

SEQ ID NO:	Name	GenBank Homology	Organism
1545	2254-6	Fo-ATP synthase subunit b	<i>D. melanogaster</i>
1546	2254-13	similar to Arabidopsis thaliana male sterility protein 2	<i>C. elegans</i>
1547	2254-17	CLN3 protein	<i>H. sapiens</i>
1548	2254-21	YbgG	<i>B. subtilis</i>
1549	2254-25	peroxisomal protein	<i>Synechocystis sp</i>
1550	2254-27	Glutaminase	<i>Rattus norvegicus</i>
1551	2254-30	tartan protein	<i>D. melanogaster</i>
1552	2254-33	leucine zipper-EF-hand containing transmembrane protein 1	<i>H. sapiens</i>
1553	2254-39	similar to helicase	<i>C. elegans</i>
1554	2254-43	muscle myosin heavy chain	<i>D. melanogaster</i>
1555	2254-45	putative nicotinate phosphoribosyltransferase	<i>N. tabacum</i>
1556	2254-51	60S ribosomal protein	<i>Mus musculus</i>
1557	2254-54	small nuclear riboprotein Sm-D	<i>H. sapiens</i>
1558	2254-55	nucleoside diphosphate kinase	<i>Salmo salar</i>
1559	2254-60	serine protease	<i>C. felis</i>
1560	2254-63	myospheroid protein	<i>D. melanogaster</i>
1561	2254-65	Carboxylesterase	<i>Anisopteromalus calandrae</i>
1562	2254-66	siah binding protein 1	<i>H. sapiens</i>
1563	2254-70	vacuolar ATPase, subunit M9.7	<i>Manduca sexta</i>
1564	2254-83	Fumarylacetoacetate hydrolase	<i>Rattus norvegicus</i>
1565	2254-84	metalloproteinase 1	<i>Hydra vulgaris</i>
1566	2254-88	alpha-spectrin	<i>D. melanogaster</i>
1567	2254-93	NADH dehydrogenase subunit 6	<i>D. melanogaster</i>
1568	2254-96	cyclophilin isoform 5	<i>C. elegans</i>
1569	2255-5	similar to mitochondrial ATPase inhibitors	<i>C. elegans</i>
1570	2255-8	yk391f12.5	<i>C. elegans</i>
1571	2255-12	Unknown	<i>H. sapiens</i>
1572	2255-17	ribonucleotide reductase subunit M1	<i>M. musculus</i>
1573	2255-19	docking protein	<i>H. sapiens</i>
1574	2255-22	Similar to rat 5E5 antigen	<i>H. sapiens</i>
1575	2255-23	ribosomal protein S31	<i>D., melanogaster</i>
1576	2255-25	Similar to acyl-CoA dehydrogenase	<i>C. elegans</i>
1577	2255-28	Arginine tyrosine kinase	<i>H. sapiens</i>
1578	2255-32	ribosomal protein L7a	<i>D., melanogaster</i>
1579	2255-33	chS-Rex-s	<i>G. gallus</i>
1580	2255-39	Phosphoacetylglucosamine mutase	<i>C. elegans</i>
1581	2255-41	NADH dehydrogenase subunit 6	<i>D., melanogaster</i>
1582	2255-45	tRNA-glutamine synthetase	<i>C. elegans</i>
1583	2255-46	p68	<i>M. musculus</i>
1584	2255-49	ABC8	<i>M. musculus</i>
1585	2255-50	kynurenine aminotransferase	<i>R. rattus</i>
1586	2255-51	SmD homolog {Gly-Arg repeat}	<i>M. musculus</i>
1587	2255-56	epoxide hydrolase	<i>S. scrofa</i>
1588	2255-60	Sec23 protein	<i>H. sapiens</i>
1589	2255-62	HMG CoA synthase	<i>M. musculus</i>
1590	2255-63	dipeptidyl aminopeptidase-like protein 6	<i>M. musculus</i>

Table II (cont'd)

SEQ ID NO:	Name	GenBank Homology	Organism
1591	2255-66	retinal rod Na ⁺ /Ca ⁺ , K ⁺ exchanger	<i>H. sapiens</i>
1592	2255-67	4-hydroxybutyrate coenzyme A transferase	<i>C. elegans</i>
1593	2255-70	hD54+ins2 isoform	<i>H. sapiens</i>
1594	2255-73	chromaffin granule ATPase II homolog	<i>M. musculus</i>
1595	2255-77	40S ribosomal protein S10	<i>H. sapiens</i>
1596	2255-79	34/67 kD laminin binding protein	<i>S. purpuratus</i>
1597	2255-82	RNA-binding protein lark	<i>D., melanogaster</i>
1598	2255-86	thiol-specific antioxidant protein	<i>R. norvegicus</i>
1599	2256-7	Similar to Human estrogen-responsive finger protein	<i>H. sapiens</i>
1600	2256-11	Trypsin	<i>C. felis</i>
1601	2256-12	CEV14	<i>H. sapiens</i>
1602	2256-16	AL021475	<i>C. elegans</i>
1603	2256-21	Heterogenous Nuclear Ribonucleoprotein C1	<i>H. sapiens</i>
1604	2256-22	b4 integrin interactor	<i>H. sapiens</i>
1605	2256-28	testis enhanced gene transcript protein	<i>H. sapiens</i>
1606	2256-31	synaptic vesicle protein 2B	<i>R. norvegicus</i>
1607	2256-40	TNF-alpha stimulated ABC protein	<i>H. sapiens</i>
1608	2256-42	carboxypeptidase A	<i>H. armigera</i>
1609	2256-46	pherophorin S	<i>V. carteri</i>
1610	2256-52	Fo-ATP synthase subunit b	<i>D. melanogaster</i>
1611	2256-54	PDGF associated protein	<i>H. sapiens</i>
1612	2256-58	S20 ribosomal protein	<i>D. melanogaster</i>
1613	2256-64	ribosomal protein S9	<i>H. sapiens</i>
1614	2256-69	elongation factor 1-gamma	<i>Artemia sp</i>
1615	2256-70	conserved hypothetical protein	<i>S. pombe</i>
1616	2256-72	fructose 1,6 bisphosphate-aldolase 4C	<i>D. melanogaster</i>
1617	2256-73	troponin-T	<i>D. melanogaster</i>
1618	2256-80	SRP14	<i>C. familiaris</i>
1619	2256-82	succinyl-CoA synthetase alpha subunit	<i>S. scrofa</i>
1620	2256-89	Csa-19	<i>H. sapiens</i>
1621	2256-92	Sacm21	<i>M. musculus</i>
1622	2256-94	apoptosis inhibitor	<i>Cydia pomonella</i> <i>granulosis virus</i>
1623	2256-96	ribosomal protein L22	<i>D. melanogaster</i>

Table III represents a variety of flea HNC nucleic acid molecules of the present invention.

Table III

SEQ ID NO:	Name
567	2096-19NB.HNC
568	2096-25NB.HNC
569	2096-48NB.HNC
570	2096-50NB.HNC
571	2096-52NB.HNC
572	2096-55NB.HNC
573	2097-09NB.HNC
574	2097-15NB.HNC
575	2097-20NB.HNC
576	2097-22NB.HNC
577	2097-32NB.HNC
578	2097-45NB.HNC
579	2097-46NB.HNC
580	2097-47NB.HNC
581	2097-56NB.HNC
582	2097-64NB.HNC
583	2098-04NB.HNC
584	2098-40NB.HNC
585	2098-43NB.HNC
586	2099-9NB.HNC
587	2100-10NB.HNC
588	2100-45NB.HNC
589	2100-47NB.HNC
590	2100-56NB.HNC
591	2100-63NB.HNC
592	2110-41NB.HNC
593	2110-53NB.HNC
594	2112-12NB.HNC
595	2112-35NB.HNC
596	2113-17NB.HNC
597	2115-16NB.HNC
598	2115-22NB.HNC
599	2115-3NB.HNC
600	2116-19NB.HNC

SEQ ID NO:	Name
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602	2116-27NB.HNC
603	2116-41NB.HNC
604	2116-59NB.HNC
605	2116-64NB.HNC
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607	2117-09NB.HNC
608	2117-11NB.HNC
609	2117-53NB.HNC
610	2118-03NB.HNC
611	2122-39NB.HNC
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613	2124-40NB.HNC
614	2124-62NB.HNC
615	2131-22NB.HNC
616	2131-32NB.HNC
617	2132-15NB.HNC
618	2132-28NB.HNC
619	2132-63NB.HNC
620	2132-9NB.HNC
621	2137-19NB.HNC
622	2137-24NB.HNC
623	2138-05NB.HNC
624	2138-51NB.HNC
625	2139-31NB.HNC
626	2139-41NB.HNC
627	2139-60NB.HNC
628	2140-13NB.HNC
629	2140-15NB.HNC
630	2140-18NB.HNC
631	2140-54NB.HNC
632	2141-16NB.HNC
633	2141-59NB.HNC
634	2142-16NB.HNC

Table III (cont'd)

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644	2168-82NB.HNC
645	2170-04NB.HNC
646	2170-08NB.HNC
647	2170-82NB.HNC
648	2172-39NB.HNC
649	2172-59NB.HNC
650	2172-60NB.HNC
651	2172-77NB.HNC
652	2174-14NB.HNC
653	2174-17NB.HNC
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660	2176-47NB.HNC
661	2176-56NB.HNC
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664	2176-64NB.HNC
665	2176-65NB.HNC
666	2176-75NB.HNC
667	2178-05NB.HNC
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670	2178-25NB.HNC
671	2178-41NB.HNC
672	2178-56NB.HNC
673	2178-57NB.HNC

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680	2178-91NB.HNC
681	2178-95NB.HNC
682	2180-05NB.HNC
683	2180-18NB.HNC
684	2180-20NB.HNC
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686	2180-59NB.HNC
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688	2180-74NB.HNC
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690	2180-79NB.HNC
691	2180-88NB.HNC
692	2180-90NB.HNC
693	2182-07NB.HNC
694	2182-12NB.HNC
695	2182-13NB.HNC
696	2182-27NB.HNC
697	2182-2NB.HNC
698	2182-46NB.HNC
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700	2182-57NB.HNC
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702	2182-64NB.HNC
703	2182-83NB.HNC
704	2182-86NB.HNC
705	2182-88NB.HNC
706	2182-90NB.HNC
707	2182-92NB.HNC
708	2182-94NB.HNC
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710	2184-37NB.HNC
711	2184-65NB.HNC
712	2186-14NB.HNC

Table III (cont'd)

SEQ ID NO:	Name
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719	2186-68NB.HNC
720	2186-69NB.HNC
721	2211-19NB.HNC
722	2211-23NB.HNC
723	2211-29NB.HNC
724	2211-30NB.HNC
725	2211-43NB.HNC
726	2211-52NB.HNC
727	2211-64NB.HNC
728	2212-30NB.HNC
729	2212-31NB.HNC
730	2212-71NB.HNC
731	2212-72NB.HNC
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733	2212-81NB.HNC
734	2212-85NB.HNC
735	2212-87NB.HNC
736	2212-91NB.HNC
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738	2212-9NB.HNC
739	2213-08NB.HNC
740	2213-09NB.HNC
741	2213-11NB.HNC
742	2213-12NB.HNC
743	2213-18NB.HNC
744	2213-34NB.HNC
745	2213-53NB.HNC
746	2213-58NB.HNC
747	2213-67NB.HNC
748	2213-79NB.HNC
749	2214-02NB.HNC
750	2214-03NB.HNC
751	2214-05NB.HNC

SEQ ID NO:	Name
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754	2214-23NB.HNC
755	2214-30NB.HNC
756	2214-36NB.HNC
757	2214-37NB.HNC
758	2214-40NB.HNC
759	2214-43NB.HNC
760	2214-53NB.HNC
761	2214-57NB.HNC
762	2214-60NB.HNC
763	2214-61NB.HNC
764	2214-73NB.HNC
765	2214-76NB.HNC
766	2214-80NB.HNC
767	2215-07NB.HNC
768	2215-15NB.HNC
769	2215-31NB.HNC
770	2215-41NB.HNC
771	2215-51NB.HNC
772	2215-80NB.HNC
773	2215-85NB.HNC
774	2215-91NB.HNC
775	2217-14NB.HNC
776	2217-16NB.HNC
777	2217-33NB.HNC
778	2217-39NB.HNC
779	2217-78NB.HNC
780	2217-92NB.HNC
781	2218-15NB.HNC
782	2218-19NB.HNC
783	2218-26NB.HNC
784	2218-36NB.HNC
785	2218-41NB.HNC
786	2218-56NB.HNC
787	2218-58NB.HNC
788	2218-69NB.HNC
789	2218-71NB.HNC
790	2218-76NB.HNC

Table III (cont'd)

SEQ ID NO:	Name
791	2218-77NB.HNC
792	2218-84NB.HNC
793	2218-96NB.HNC
794	2219-11NB.HNC
795	2219-13NB.HNC
796	2219-17NB.HNC
797	2219-19NB.HNC
798	2219-20NB.HNC
799	2219-22NB.HNC
800	2219-23NB.HNC
801	2219-32NB.HNC
802	2219-45NB.HNC
803	2219-49NB.HNC
804	2219-51NB.HNC
805	2219-72NB.HNC
806	2219-80NB.HNC
807	2219-952122-39NB.HNC
	2220-02NB.HNC
808	2220-02NB.HNC
809	2220-27NB.HNC
810	2220-32NB.HNC
811	2220-53NB.HNC
812	2220-60NB.HNC
813	2220-66NB.HNC
814	2221-06NB.HNC
815	2221-15NB.HNC
816	2221-18NB.HNC
817	2221-20NB.HNC
818	2221-24NB.HNC
819	2221-45NB.HNC
820	2221-46NB.HNC
821	2221-48NB.HNC
822	2221-54NB.HNC
823	2221-55NB.HNC
824	2221-59NB.HNC
825	2221-61NB.HNC
826	2221-62NB.HNC
827	2221-70NB.HNC
828	2221-86NB.HNC

SEQ ID NO:	Name
829	2221-87NB.HNC
830	2221-95NB.HNC
831	2223u-18NB.HNC
832	2223u-22NB.HNC
833	2223u-23NB.HNC
834	2223u-31NB.HNC
835	2223u-33NB.HNC
836	2223u-36NB.HNC
837	2223u-67NB.HNC
838	2223u-85NB.HNC
839	2224u-05NB.HNC
840	2224u-07NB.HNC
841	2224u-10NB.HNC
842	2224u-11NB.HNC
843	2224u-15NB.HNC
844	2224u-25NB.HNC
845	2224u-27NB.HNC
846	2224u-44NB.HNC
847	2224u-52NB.HNC
848	2224u-62NB.HNC
849	2224u-70NB.HNC
850	2224u-71NB.HNC
851	2224u-79NB.HNC
852	2225u-11NB.HNC
853	2225u-20NB.HNC
854	2225u-23NB.HNC
855	2225u-28NB.HNC
856	2225u-55NB.HNC
857	2225u-59NB.HNC
858	2225u-64NB.HNC
859	2225u-77NB.HNC
860	2225u-95NB.HNC
861	2226-932122-39NB.HNC
862	2226u-07NB.HNC
863	2226u-19NB.HNC
864	2226u-39NB.HNC
865	2226u-45NB.HNC
866	2226u-49NB.HNC

Table III (cont'd)

SEQ ID NO:	Name
867	2226u-54NB.HNC
868	2226u-71NB.HNC
869	2226u-77NB.HNC
870	2226u-83NB.HNC
871	2226u-91NB.HNC
872	2227u-12NB.HNC
873	2227u-13NB.HNC
874	2227u-23NB.HNC
875	2227u-26NB.HNC
876	2227u-30NB.HNC
877	2227u-31NB.HNC
878	2227u-33NB.HNC
879	2227u-43NB.HNC
880	2227u-51NB.HNC
881	2227u-60NB.HNC
882	2227u-93NB.HNC
883	2228u-04NB.HNC
884	2228u-09NB.HNC
885	2228u-12NB.HNC
886	2228u-21NB.HNC
887	2228u-26NB.HNC
888	2228u-49NB.HNC
889	2228u-54NB.HNC
890	2228u-55NB.HNC
891	2228u-61NB.HNC
892	2228u-65NB.HNC
893	2228u-79NB.HNC
894	2228u-90NB.HNC
1624	2222-7
1625	2222-16
1626	2222-19
1627	2222-39
1628	2222-56
1629	2222-59
1630	2222-79
1631	2222-89
1632	2228-4
1633	2228-9
1634	2228-12
1635	2228-21
1636	2228-26
1637	2228-49

SEQ ID NO:	Name
1638	2228-54
1639	2228-61
1640	2228-65
1641	2228-79
1642	2228-90
1643	2245-5
1644	2245-7
1645	2245-15
1646	2245-16
1647	2245-17
1648	2245-20
1649	2245-35
1650	2245-38
1651	2245-39
1652	2245-51
1653	2245-52
1654	2245-57
1655	2246-13
1656	2246-19
1657	2246-25
1658	2246-27
1659	2246-29
1660	2246-40
1661	2246-45
1662	2246-52
1663	2246-64
1664	2246-66
1665	2246-74
1666	2246-82
1667	2247-6
1668	2247-17
1669	2247-29
1670	2247-31
1671	2247-36
1672	2247-40
1673	2247-46
1674	2247-50
1675	2247-54
1676	2247-63
1677	2247-66
1678	2247-68
1679	2247-69
1680	2247-81
1681	2247-82
1682	2247-95
1683	2248-7

Table III (cont'd)

SEQ ID NO:	Name
1684	2248-18
1685	2248-32
1686	2248-41
1687	2248-50
1688	2248-54
1689	2248-60
1690	2248-62
1691	2248-65
1692	2248-86
1693	2248-94
1694	2249-6
1695	2249-30
1696	2249-35
1697	2249-36
1698	2249-68
1699	2249-74
1700	2249-79
1701	2250-20
1702	2250-24
1703	2251-7
1704	2251-21
1705	2251-25
1706	2251-38
1707	2251-58
1708	2252-7
1709	2252-15
1710	2252-19
1711	2252-24
1712	2252-26
1713	2252-27
1714	2252-32
1715	2252-36
1716	2252-37
1717	2252-69
1718	2252-78

Table IV represents a variety of flea HMT nucleic acid molecules of the present invention.

Table IV

SEQ ID NO:	Name
895	2084-02.HMTNB
896	2084-05.HMTNB
897	2084-07.HMTNB
898	2084-09.HMTNB
899	2084-15.HMTNB
900	2084-17.HMTNB
901	2084-18.HMTNB
902	2084-21.HMTNB
903	2084-22.HMTNB
904	2084-30.HMTNB
905	2084-33.HMTNB
906	2084-36.HMTNB
907	2084-37.HMTNB
908	2084-38.HMTNB
909	2084-39.HMTNB
910	2084-43.HMTNB
911	2084-50.HMTNB
912	2084-54.HMTNB
913	2084-56.HMTNB
914	2084-59.HMTNB
915	2085-03.HMTNB
916	2085-13.HMTNB
917	2085-35.HMTNB
918	2085-38.HMTNB
919	2085-39.HMTNB
920	2085-49.HMTNB
921	2085-53.HMTNB
922	2085-58.HMTNB
923	2085-61.HMTNB
924	2086-05.HMTNB
925	2086-10.HMTNB
926	2086-13.HMTNB
927	2086-15.HMTNB
928	2086-20.HMTNB
929	2086-25.HMTNB
930	2086-32.HMTNB
931	2086-33.HMTNB
932	2086-34.HMTNB
933	2086-37.HMTNB
934	2086-41.HMTNB
935	2086-43.HMTNB

SEQ ID NO:	Name
936	2086-44.HMTNB
937	2086-54.HMTNB
938	2086-55.HMTNB
939	2086-58.HMTNB
940	2087-09.HMTNB
941	2087-17.HMTNB
942	2087-28.HMTNB
943	2087-33.HMTNB
944	2087-35.HMTNB
945	2087-51.HMTNB
946	2087-54.HMTNB
947	2088-07.HMTNB
948	2088-17.HMTNB
949	2088-35.HMTNB
950	2088-52.HMTNB
951	2088-59.HMTNB
952	2089-12.HMTNB
953	2089-14.HMTNB
954	2089-33.HMTNB
955	2089-36.HMTNB
956	2089-51.HMTNB
957	2089-60.HMTNB
958	2090-11.HMTNB
959	2090-27.HMTNB
960	2090-33.HMTNB
961	2090-44.HMTNB
962	2090-57.HMTNB
963	2091-11.HMTNB
964	2091-22.HMTNB
965	2091-23.HMTNB
966	2091-35.HMTNB
967	2091-63.HMTNB
968	2092-11.HMTNB
969	2092-16.HMTNB
970	2092-40.HMTNB
971	2092-42.HMTNB
972	2092-46.HMTNB
973	2092-60.HMTNB
974	2093-20.HMTNB
975	2093-23.HMTNB
976	2093-43.HMTNB

Table IV (cont'd)

SEQ ID NO:	Name
977	2093-48.HMTNB
978	2093-50.HMTNB
979	2093-62.HMTNB
980	2093-63.HMTNB
981	2094-08.HMTNB
982	2094-26.HMTNB
983	2094-33.HMTNB
984	2094-47.HMTNB
985	2094-50.HMTNB
986	2094-62.HMTNB
987	2095-04.HMTNB
988	2095-10.HMTNB
989	2095-12.HMTNB
990	2095-13.HMTNB
991	2095-15.HMTNB
992	2095-20.HMTNB
993	2095-22.HMTNB
994	2095-31.HMTNB
995	2095-33.HMTNB
996	2095-34.HMTNB
997	2095-36.HMTNB
998	2095-40.HMTNB
999	2095-48.HMTNB
1000	2102-12.HMTNB
1001	2102-16.HMTNB
1002	2102-18.HMTNB
1003	2102-19.HMTNB
1004	2102-20.HMTNB
1005	2102-29.HMTNB
1006	2102-35.HMTNB
1007	2102-37.HMTNB
1008	2102-38.HMTNB
1009	2102-41.HMTNB
1010	2102-47.HMTNB
1011	2103-02.HMTNB
1012	2103-09.HMTNB
1013	2103-45.HMTNB
1014	2103-56.HMTNB
1015	2103-58.HMTNB
1016	2104-58.HMTNB
1017	2104-60.HMTNB
1018	2104-61.HMTNB
1019	2105-02.HMTNB
1020	2105-20.HMTNB
1021	2105-35.HMTNB
1022	2105-42.HMTNB
1023	2105-44.HMTNB
1024	2106-05.HMTNB

SEQ ID NO:	Name
1025	2106-27.HMTNB
1026	2106-29.HMTNB
1027	2106-34.HMTNB
1028	2106-48.HMTNB
1029	2106-50.HMTNB
1030	2106-64.HMTNB
1031	2107-02.HMTNB
1032	2107-10.HMTNB
1033	2107-37.HMTNB
1034	2108-03.HMTNB
1035	2108-23.HMTNB
1036	2108-46.HMTNB
1037	2108-47.HMTNB
1038	2108-48.HMTNB
1039	2108-49.HMTNB
1040	2108-63.HMTNB
1041	2109-04.HMTNB
1042	2109-06.HMTNB
1043	2109-37.HMTNB
1044	2109-38.HMTNB
1045	2109-44.HMTNB
1046	2154-08.HMTNB
1047	2154-09.HMTNB
1048	2154-10.HMTNB
1049	2154-28.HMTNB
1050	2154-30.HMTNB
1051	2154-45.HMTNB
1052	2154-46.HMTNB
1053	2154-61.HMTNB
1054	2154-71.HMTNB
1055	2154-81.HMTNB
1056	2154-83.HMTNB
1057	2156-02.HMTNB
1058	2156-06.HMTNB
1059	2156-18.HMTNB
1060	2156-27.HMTNB
1061	2156-43.HMTNB
1062	2156-48.HMTNB
1063	2156-50.HMTNB
1064	2157-16.HMTNB
1065	2157-34.HMTNB
1066	2157-45.HMTNB
1067	2157-70.HMTNB
1068	2157-75.HMTNB
1069	2157-79.HMTNB
1070	2157-86.HMTNB
1071	2158-02.HMTNB
1072	2158-14.HMTNB

Table IV (cont'd)

SEQ ID NO:	Name
1073	2158-19.HMTNB
1074	2158-22.HMTNB
1075	2158-27.HMTNB
1076	2158-34.HMTNB
1077	2158-37.HMTNB
1078	2158-39.HMTNB
1079	2159-07.HMTNB
1080	2159-09.HMTNB
1081	2159-17.HMTNB
1082	2159-34.HMTNB
1083	2159-35.HMTNB
1084	2159-60.HMTNB
1085	2160-16.HMTNB
1086	2160-17.HMTNB
1087	2160-29.HMTNB
1088	2160-30.HMTNB
1089	2160-32.HMTNB
1090	2160-39.HMTNB
1091	2160-49.HMTNB
1092	2160-53.HMTNB
1093	2160-54.HMTNB
1094	2160-55.HMTNB
1095	2160-77.HMTNB
1096	2160-82.HMTNB
1097	2160-89.HMTNB
1098	2160-91.HMTNB
1099	2161-13.HMTNB
1100	2161-19.HMTNB
1101	2161-45.HMTNB
1102	2161-57.HMTNB
1103	2161-60.HMTNB
1104	2161-79.HMTNB
1105	2161-83.HMTNB
1106	2161-90.HMTNB
1107	2161-94.HMTNB
1108	2162-05.HMTNB
1109	2162-12.HMTNB
1110	2162-13.HMTNB
1111	2162-18.HMTNB
1112	2162-35.HMTNB
1113	2162-41.HMTNB
1114	2162-50.HMTNB
1115	2162-59.HMTNB
1116	2162-63.HMTNB
1117	2162-71.HMTNB
1118	2162-75.HMTNB
1119	2162-78.HMTNB
1120	2163-07.HMTNB

SEQ ID NO:	Name
1121	2163-11.HMTNB
1122	2163-18.HMTNB
1123	2163-23.HMTNB
1124	2163-25.HMTNB
1125	2163-43.HMTNB
1126	2163-50.HMTNB
1127	2163-61.HMTNB
1128	2163-65.HMTNB
1129	2163-73.HMTNB
1130	2163-77.HMTNB
1131	2163-87.HMTNB
1132	2163-93.HMTNB
1133	2163-95.HMTNB
1134	2165-04.HMTNB
1135	2165-06.HMTNB
1136	2165-24.HMTNB
1137	2165-45.HMTNB
1138	2165-59.HMTNB
1139	2165-65.HMTNB
1140	2166-02.HMTNB
1141	2166-12.HMTNB
1142	2166-42.HMTNB
1143	2166-46.HMTNB
1144	2166-47.HMTNB
1145	2167-07.HMTNB
1146	2167-16.HMTNB
1147	2167-42.HMTNB
1148	2167-65.HMTNB
1149	2167-66.HMTNB
1150	2167-79.HMTNB
1151	2167-90.HMTNB
1152	2167-94.HMTNB
1153	2169-05.HMTNB
1154	2169-12.HMTNB
1155	2169-16.HMTNB
1156	2169-17.HMTNB
1157	2169-19.HMTNB
1158	2169-22.HMTNB
1159	2169-26.HMTNB
1160	2169-33.HMTNB
1161	2169-42.HMTNB
1162	2169-46.HMTNB
1163	2169-47.HMTNB
1164	2169-57.HMTNB
1165	2169-69.HMTNB
1166	2171-06.HMTNB
1167	2171-09.HMTNB
1168	2171-11.HMTNB

Table IV (cont'd)

SEQ ID NO:	Name
1169	2171-29.HMTNB
1170	2171-33.HMTNB
1171	2171-35.HMTNB
1172	2171-41.HMTNB
1173	2171-54.HMTNB
1174	2171-57.HMTNB
1175	2171-69.HMTNB
1176	2171-82.HMTNB
1177	2171-84.HMTNB
1178	2171-85.HMTNB
1179	2173-12.HMTNB
1180	2173-34.HMTNB
1181	2173-42.HMTNB
1182	2173-48.HMTNB
1183	2173-54.HMTNB
1184	2173-57.HMTNB
1185	2173-75.HMTNB
1186	2173-86.HMTNB
1187	2173-91.HMTNB
1188	2175-06.HMTNB
1189	2175-15.HMTNB
1190	2175-20.HMTNB
1191	2175-58.HMTNB
1192	2175-96.HMTNB
1193	2177-16.HMTNB
1194	2177-70.HMTNB
1195	2177-86.HMTNB
1196	2179-02.HMTNB
1197	2179-03.HMTNB
1198	2179-19.HMTNB
1199	2179-22.HMTNB
1200	2179-29.HMTNB
1201	2179-39.HMTNB
1202	2179-63.HMTNB
1203	2181-04.HMTNB
1204	2181-24.HMTNB
1205	2181-35.HMTNB
1206	2181-66.HMTNB
1207	2181-75.HMTNB
1208	2181-76.HMTNB
1209	2181-84.HMTNB
1210	2183-05.HMTNB
1211	2183-13.HMTNB
1212	2183-17.HMTNB
1213	2183-28.HMTNB
1214	2183-45.HMTNB
1215	2183-50.HMTNB
1216	2183-51.HMTNB

SEQ ID NO:	Name
1217	2183-70.HMTNB
1218	2185-05.HMTNB
1219	2185-10.HMTNB
1220	2185-12.HMTNB
1221	2185-18.HMTNB
1222	2185-43.HMTNB
1223	2185-49.HMTNB
1224	2185-54.HMTNB
1225	2185-82.HMTNB
1226	2187-21.HMTNB
1227	2187-37.HMTNB
1228	2187-47.HMTNB
1229	2187-93.HMTNB
1230	2188-22.HMTNB
1231	2188-29.HMTNB
1232	2188-32.HMTNB
1233	2188-52.HMTNB
1234	2188-54.HMTNB
1235	2188-72.HMTNB
1236	2188-92.HMTNB
1237	2189-31.HMTNB
1238	2189-56.HMTNB
1239	2189-75.HMTNB
1240	2189-84.HMTNB
1241	2191-23.HMTNB
1242	2191-38.HMTNB
1243	2191-58.HMTNB
1244	2191-73.HMTNB
1245	2191-77.HMTNB
1246	2191-90.HMTNB
1247	2191-94.HMTNB
1248	2191-96.HMTNB
1249	2192-03.HMTNB
1250	2192-14.HMTNB
1251	2192-36.HMTNB
1252	2192-46.HMTNB
1253	2192-88.HMTNB
1254	2194-07.HMTNB
1255	2194-13.HMTNB
1256	2194-16.HMTNB
1257	2194-18.HMTNB
1258	2194-28.HMTNB
1259	2195-06.HMTNB
1260	2195-47.HMTNB
1261	2195-60.HMTNB
1262	2196-18.HMTNB
1263	2196-30.HMTNB
1264	2196-53.HMTNB

Table IV (cont'd)

SEQ ID NO:	Name
1265	2196-65.HMTNB
1266	2196-76.HMTNB
1267	2197-28.HMTNB
1268	2197-46.HMTNB
1269	2197-51.HMTNB
1270	2197-59.HMTNB
1271	2202-96.HMTNB
1272	2203-36.HMTNB
1273	2204-09.HMTNB
1274	2205-11.HMTNB
1275	2205-33.HMTNB
1276	2205-43.HMTNB
1277	2205-85.HMTNB
1278	2229-08u.HMTNB
1279	2229-10u.HMTNB
1280	2229-12u.HMTNB
1281	2229-14u.HMTNB
1282	2229-27u.HMTNB
1283	2229-40u.HMTNB
1284	2229-45u.HMTNB
1285	2229-48u.HMTNB
1286	2229-50u.HMTNB
1287	2229-54u.HMTNB
1288	2229-56u.HMTNB
1289	2229-57u.HMTNB
1290	2229-59u.HMTNB
1291	2229-70u.HMTNB
1292	2229-87u.HMTNB
1293	2229-91u.HMTNB
1294	2229-95u.HMTNB
1295	2230-07u.HMTNB
1296	2230-11u.HMTNB
1297	2230-19u.HMTNB
1298	2230-27u.HMTNB
1299	2230-33u.HMTNB
1300	2230-41u.HMTNB
1301	2230-51u.HMTNB
1302	2230-56u.HMTNB
1303	2230-66u.HMTNB
1304	2230-71u.HMTNB
1305	2230-75.HMTNB
1306	2230-81u.HMTNB
1307	2230-84u.HMTNB
1308	2230-93u.HMTNB
1309	2231-23u.HMTNB
1310	2231-26u.HMTNB
1311	2231-32u.HMTNB
1312	2231-37u.HMTNB

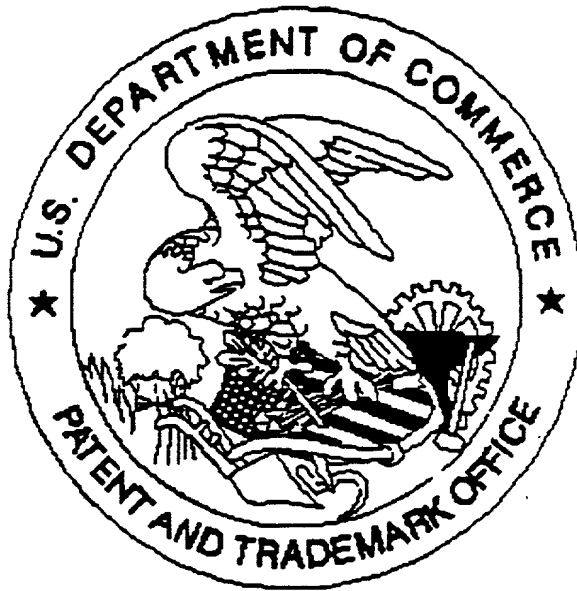
SEQ ID NO:	Name
1313	2231-44u.HMTNB
1314	2231-50u.HMTNB
1315	2231-51u.HMTNB
1316	2231-63u.HMTNB
1317	2231-68u.HMTNB
1318	2231-74u.HMTNB
1319	2231-82u.HMTNB
1320	2231-85u.HMTNB
1321	2231-88u.HMTNB
1322	2231-94u.HMTNB
1323	2231-95u.HMTNB
1324	2232-03u.HMTNB
1325	2232-11u.HMTNB
1326	2232-19u.HMTNB
1327	2232-25u.HMTNB
1328	2232-30u.HMTNB
1329	2232-44u.HMTNB
1330	2232-50u.HMTNB
1331	2232-56u.HMTNB
1332	2232-60u.HMTNB
1333	2232-64u.HMTNB
1334	2232-71u.HMTNB
1335	2232-73u.HMTNB
1336	2232-80u.HMTNB
1337	2232-83u.HMTNB
1338	2233-02u.HMTNB
1339	2233-53u.HMTNB
1340	2233-57u.HMTNB
1341	2233-58u.HMTNB
1342	2233-80u.HMTNB
1343	2233-81u.HMTNB
1344	2233-83u.HMTNB
1345	2234-02u.HMTNB
1346	2234-03u.HMTNB
1347	2234-05u.HMTNB
1348	2234-06u.HMTNB
1349	2234-09u.HMTNB
1350	2234-12u.HMTNB
1351	2234-23u.HMTNB
1352	2234-26u.HMTNB
1353	2234-46u.HMTNB
1354	2234-66u.HMTNB
1355	2234-67u.HMTNB
1356	2234-70u.HMTNB
1357	2234-74u.HMTNB
1358	2234-77u.HMTNB
1359	2234-82u.HMTNB
1360	2234-88u.HMTNB

Table IV (cont'd)

SEQ ID NO:	Name
1361	2234-89u.HMTNB
1362	2234-90u.HMTNB
1363	2234-93u.HMTNB
1364	2240-39
1365	2240-40
1366	2240-49
1367	2240-51
1368	2240-57
1369	2240-61
1370	2240-62
1371	2241-2
1372	2241-3
1373	2241-8
1374	2241-9
1375	2241-13
1376	2241-21
1377	2241-29
1378	2241-38
1379	2241-45
1380	2241-49
1381	2241-51
1382	2241-57
1383	2241-63
1384	2241-68
1385	2241-89
1386	2241-91
1387	2243-2
1388	2243-3
1389	2243-12
1390	2243-14
1391	2243-19
1392	2243-24
1393	2243-25
1394	2243-33
1395	2243-49
1396	2243-50
1397	2243-51
1398	2243-59
1399	2243-63
1400	2243-69
1401	2243-74
1402	2243-75
1403	2243-77
1404	2244-19
1405	2244-26
1406	2244-35
1407	2244-38
1408	2244-40

SEQ ID NO:	Name
1409	2244-47
1410	2244-52
1411	2244-57
1412	2244-63
1413	2244-68
1414	2244-77
1415	2244-80

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for scanning. (Document title)

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for scanning. (Document title)

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specifications were Tables.*